Raw Sequence Listing

12/16/92 09:44:55 S4267.raw

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SEQUENCE LISTING See Pr. 1,44 -> 16
 2
 3
 4
    (1) GENERAL INFORMATION
 5
 6
    (i) APPLICANT: Darrell Anderson, Nabil Hanna, John Leonard, Roland Newman and Mitchell R
 7
 8
    (ii) TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC ANTIBODY TO HUMAN B LYMPHOCY
 9
10
    (iii) NUMBER OF SEQUENCES: 8
11
12
    (iv) CORRESPONDING ADDRESS:
13
    (A) ADDRESSEE: IDEC Pharmaceuticals Corporation
14
15
    (B)STREET:11099 N. Torrey Pines Road, #160
    (C)CITY:La Jolla
16
17
    (D)STATE: California
    (E) COUNTRY: USA
19
    (F)ZIP:92037
20
21
    (v) COMPUTER READABLE FORM:
22
23
    (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
24
    (B) COMPUTER: Macintosh
25
    (C) OPERATING SYSTEM: MS.DOS
    (D) SOFTWARE: Microsoft Word 5.0
26
                                              parenthes!s
27
28
    (viCURRENT APPLICATION DATA:
29
30
    (A) APPLICATION NUMBER:
    (B) FILING DATE:
31
32
    (C) CLASSIFICATION:
33
34
    (viii) ATTORNEY/AGENT INFORMATION:
                                    De lete (Edit provision)

1:
35
36
    (A) NAME: Burgoon, Richard P. Jr.
37
    (B) REGISTRATION NUMBER: 34,787
38
    (C) REFERENCE/DOCKET NUMBER:
39
40
    (ix) TELECOMMUNICATION INFORMATION:
41
42
    (A) TELEPHONE: (619) 458-0600
43
    (B) TELEFAX: (619) 546-9274
44
45
   (2) INFORMATION FOR SEQ. ID NO.:
46
47
48
    (i) SEQUENCE CHARACTERISTICS:
49
50
   (A)LENGTH: 8540 bases
    (B) TYPE: nucleic acid
51
    (C)STRANDEDNESS: single
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PAGE:

792

797

812

1

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/07/978,891

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LINE ORIGINAL TEXT

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(ix) SEQUENCE DESCRIPTION: SEQ. ID. NO.:

(ix) SEQUENCE DESCRIPTION: SEQ. ID. NO.:

(9) INFORMATION FOR SEQ. ID. NO.: 8:

CORRECTED TEXT

(1) GENERAL INFORMATION:		
(iv) CORRESPONDENCE ADDRESS:		
(2) INFORMATION FOR SEQ ID NO:	1:	
(ix) SEQUENCE DESCRIPTION: SEQ	ID.	NO:
(2) INFORMATION FOR SEQ ID NO:	2:	
(ix) SEQUENCE DESCRIPTION: SEQ	ID.	NO:
(2) INFORMATION FOR SEQ ID NO:	3:	
(ix) SEQUENCE DESCRIPTION: SEQ	ID.	NO:
(2) INFORMATION FOR SEQ ID NO:	4:	
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(2) INFORMATION FOR SEQ ID NO:	7:	
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(2) INFORMATION FOR SEQ ID NO:	8:	
(ix) SEQUENCE DESCRIPTION: SEQ	ID.	NO:

PAGE: 1

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/07/978,891

DATE: 12/16/92 TIME: 09:46:26

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MANDATORY IDENTIFIER THAT WAS NOT FOUND

CURRENT APPLICATION DATA
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/07/978,891

DATE: 12/16/92 TIME: 09:46:26

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LINE ERROR

ORIGINAL TEXT

(vidurent application data:

28	Response Exceeds Line Limitations
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31	Unknown or Misplaced Identifier
32	Unknown or Misplaced Identifier
695	Wrong Nucleic Acid Designator
692	Entered and Calc. Seq. Length differ
716	Wrong Nucleic Acid Designator
734	Entered and Calc. Seq. Length differ
772	Wrong Nucleic Acid Designator
794	Wrong Nucleic Acid Designator
792	Entered and Calc. Seq. Length differ

812 Entered and Calc. Seq. Length differ

(A)APPLICATION NUMBER:
(B)FILING DATE:
_(C)*CLASSIFICATION:
TC 3' 2
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5' GG(G/C) TGT TGT GCT AGC TG(A/C) (A/G)
(ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.:
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Patent Application US/07/978,891

53 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

(iv)ANTI-SENSE: no

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ATGGTTGCTG	ACTAATTGAG	ATGCATGCTT	TGCATACTTC	TGCCTGCTGG	GGAGCCTGGG	240
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CGGTGGGAGG	TCTATATAAG	CAGAGCTGGG	TACGTGAACC	GTCAGATCGC	CTGGAGACGC	960
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CTCCCAGGTG	CACGATGTGA	TGGTACCAAG	GTGGAAATCA	AACGTACGGT	GGCTGCACCA	1080
TCTGTCTTCA	TCTTCCCGCC	ATCTGATGAG	CAGTTGAAAT	CTGGAACTGC	CTCTGTTGTG	1140
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TGTTGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCGT GACAACATGC 1440 110 111 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1500 112 113 GTTTGCCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCCTTTCC 1560 114 115 TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620 116 117 GGGGTGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680 118 119 GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 1740 120 121 ACGTCAATGA CGGTAAATGG CCCGCCTGC ATTATGCCCA GTACATGACC TTATGGGACT 1800 122 123 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 1860 124 125 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC 1920 126 127 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980 128 129 GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
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110 111 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1500 112 113 GTTTGCCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCCTTTCC 1560 114 115 TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620 116 117 GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680 118 119 GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 1740 120 121 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 1800 122 123 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 1860 124 125 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC 1920 126 127 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980 128 129 GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
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112 113 GTTTGCCCCT CCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCCTTTCC 1560 114 115 TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620 116 117 GGGGTGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680 118 119 GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 1740 120 121 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 1800 122 123 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 1860 124 125 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACC GGGATTTCCA AGTCTCCACC 1920 126 127 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980 128 129 GTAACAACTC CGCCCCATTG ACGCAAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
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120 121 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 1800 122 123 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 1860 124 125 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC 1920 126 127 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980 128 129 GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
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124 125 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC 1920 126 127 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980 128 129 GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC 1920 126 127 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980 128 129 GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
126 127 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980 128 129 GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
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133 ATGGGTTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG CTACGCGTGT CGCTAGCACC 2160
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137 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 2280
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148 149 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 2640
149 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 2640
151 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 2700
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153 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 2760
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155 TGCAAGGTCT CCAACAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 2820
156

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TGGGAGAGCA	ATGGGCAGCC	GGAGAACAAC	TACAAGACCA	CGCCTCCCGT	GCTGGACTCC	3000
GACGGCTCCT	TCTTCCTCTA	CAGCAAGCTC	ACCGTGGACA	AGAGCAGGTG	GCAGCAGGGG	3060
AACGTCTTCT	CATGCTCCGT	GATGCATGAG	GCTCTGCACA	ACCACTACAC	GCAGAAGAGC	3120
CTCTCCCTGT	CTCCGGGTAA	ATGAGGATCC	GTTAACGGTT	ACCAACTACC	TAGACTGGAT	3180
TCGTGACAAC	ATGCGGCCGT	GATATCTACG	TATGATCAGC	CTCGACTGTG	CCTTCTAGTT	3240
GCCAGCCATC	TGTTGTTTGC	CCCTCCCCCG	TGCCTTCCTT	GACCCTGGAA	GGTGCCACTC	3300
						3360
						3420
						3480
						3540
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AGACAGTGTT	CTCTGCACAG	ATAAGGACAA	ACATTATTCA	GAGGGAGTAC	CCAGAGCTGA	3660
GACTCCTAAG	CCAGTGAGTG	GCACAGCATT	CTAGGGAGAA	ATATGCTTGT	CATCACCGAA	3720
GCCTGATTCC	GTAGAGCCAC	ACCTTGGTAA	GGGCCAATCT	GCTCACACAG	GATAGAGAGG	3780
GCAGGAGCCA	GGGCAGAGCA	TATAAGGTGA	GGTAGGATCA	GTTGCTCCTC	ACATTTGCTT	3840
CTGACATAGT	TGTGTTGGGA	GCTTGGATAG	CTTGGACAGC	TCAGGGCTGC	GATTTCGCGC	3900
CAAACTTGAC	GGCAATCCTA	GCGTGAAGGC	TGGTAGGATT	TTATCCCCGC	TGCCATCATG	3960
GTTCGACCAT	TGAACTGCAT	CGTCGCCGTG	TCCCAAAATA	TGGGGATTGG	CAAGAACGGA	4020
GACCTACCCT	GGCCTCCGCT	CAGGAACGAG	TTCAAGTACT	TCCAAAGAAT	GACCACAACC	4080
TCTTCAGTGG	AAGGTAAACA	GAATCTGGTG	ATTATGGGTA	GGAAAACCTG	GTTCTCCATT	4140
						4200
						4260
						4320
TACCAGGAAG	CCATGAATCA	ACCAGGCCAC	CTTAGACTCT	TTGTGACAAG	GATCATGCAG	4380
	AACCAGGTCA TGGGAGAGCA GACGGCTCCT AACGTCTTCT CTCTCCCTGT TCGTGACAAC GCCAGCCATC CCACTGTCCT CTATTCTGGG GGCATCCCC AATTTTAACA AGACAGTGTT GACTCCTAAG GCCTGATTCC GCAGGAGCCA CTGACATAGT CAAACTTGAC GTTCGACCAT GACCTACCCT TCTTCAGTGG CCTGAGAAGA GAACCACCAC GAACCACCAC	AACCAGGTCA GCCTGACCTG TGGGAGAGCA ATGGGCAGCC GACGGCTCCT TCTTCCTCTA AACGTCTTCT CATGCTCCGT CTCTCCCTGT CTCCGGGTAA TCGTGACAAC ATGCGGCCGT GCCAGCCATC TGTTGTTGC CCACTGTCCT TTCCTAATAA CTATTCTGGG GGGTGGGGTG GGCATCCCC AGCTTTGCTT AATTTAACA CCAATTCAGT AGACAGTGTT CTCTGCACAG GACTCCTAAG CCAGTGAGTG GCCTGATTCC GTAGAGCCAC CTGACATAGT TGTGTTGGGA CTAACTTGAC GGCAGAGCA CTGACATAGT TGTGTTGGGA CAAACTTGAC GGCAATCCTA GTTCGACCAT TGAACTGCAT GACCTACCT GGCCTCCGCT TCTTCAGTGG AAGGTAAACA CCTGAGAAGA ATCGACCTTC GAACCACCAC GAGGAGCTCA GAACCACCAC GAGGAGCTCA	AACCAGGTCAGCCTGACCTGCCTGGTCAAATGGGAGAGCAATGGGCAGCCGGAGAACAACGACGGCTCCTTCTTCCTCTACAGCCAGCTCAACGTCTTCTCATGCTCCGTGATGCATGAGCTCTCCCTGTCTCCGGGTAAATGAGGATCCTCGTGACAACATGCGGCCGTGATATCTACGGCCAGCCATCTTCCTAATAAAATGAGGAAACTATTCTGGGGGGTGGGGTGGGCCAGGACAGGCATGCTGGGATGCGGTGGGCTCTATGGCCCGATCCCCAGCTTTGCTTCTCAATTTCTAATTTTAACACCAATTCAGTAGTTGATTGAGACAGGTGTTCTCTGCACAGATAAGGACAAGACTCCTAAGCCAGTGAGTGGCACAGCATTGCCTGATTCCGTAGAGCCACACCTTGGTAAGCAGGAGCCAGCTTGGATAGGCTTGGATAGCTGACATAGTTGTGTTGGGAGCTTGGATAGGAACCACCATGGCCTCCGCTCAGGAACGAGTCTTCAGTGGAAGGTAAACAGAATCTGGTGGCCTGAGAAGAATGACCTTTAAAGGACAGAGAACCACCACGAGGAGCTCATTTTCTTGCCGAACCACCACGAGGAGCTCATTTTCTTGCCGAACAACCACGAGGAGCTCATTTTCTTGCCGAACAACCACGAGGAGCTCATTTTCTTGCC	AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA CTCTCCCCTGT CTCCGGGTAA ATGAGGATCC GTTAACGGTT TCGTGACAAC ATGCGGCCGT GATATCTACG TATGATCAGC GCCAGCCATC TCTCTAATAA AATGAGGAAA TTGCATCGCA CCACTGTCCT TTCCTAATAA AATGAGGACA GCAAGGGGG GGCATGCTGG GGGTGGGGTG GGCCAGGACA GCAAGGGGA GCCATGCTCG AGCTTTGCTT CTCAATTTCT TATTTCCATAG AAATTTTAACA CCAATTCAGT ACTAGTTCA ACAATTATTCA AAACTACCTAAG CTCGCACATT CTAGGGAGAA ACATTATTCA GCACGGAGCA ACCTTGGTAA ACATTATTCA CTAGGAGAAA ACATTATTCA GCAGGAGCAC GCCTGGATAGC ACCTTGGTAA GGTAGGATCA ACCTTGGATAG CTTGGACATCA CTTGGACATCA CTTGGACATCA CTTGGACATCA CTTGGACATCA CT	TGGGAGAGCA ATGGGCAGC GGAGAACAAC TACAAGACCA CGCCTCCGT GACGGCTCCT TCTTCCTCTA CAGCAAGCCT ACCGTGGACA AGAGCAGGTG AACGTCTTC CATGCTCCGT GATGCATGAG GCTCTCCACA ACCACTACAC CTCTCCCTGT CTCCGGGTAA ATGAGGATC GTTAACGGTT ACCAACTACC CTCTCCCTGT CTCCGGGTAA ATGAGGATC GTTAACGGTT ACCAACTACC CTCGTGACAAC ATGCGGCCGT GATATCTACG TATGATCAGC CTCGACCAC CCACTGTCCT TTCCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT CCACTGTCCT TTCCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT CTATTCTGGG GGGTGGGGTG GGCCAGGACA GCAAGGGGGA GGATTGGGAA CCCGGATCCCC AGCTTTGCTT CTCAATTTCT TATTTGCATA ATGAGAAAAA AATTTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAAA AATTTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAAA AATTTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAAA AGACAGTGTT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGGGAGTAC GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GCAGGAGCCA GGCAGGCAA TATAAGGTGA GTTGGACAG TCCACACAG GCAGGAGCCA GGCAGGCA TATAAGGTGA GTTGGACAG TCAGGGCTGC CAAACTTGAC GGCAATCCTA GCGTGAAGG TTCGAAAAAT TGGGGATTGG GCACTACCCT GGCCTCCGCT CAGGAACGA TTCAAACAAT TGGGGATTGG GACCTACCCT GGCCTCCGCT CAGGAACGA TTCAAACTACT TCCCAAAAATA TCTTCAGTGG AAGGTAAACA GAATCTGGT ATTAATGGGTA GGAAAACCTG GCCTGAGAAGA ATGGACCAC TCAAACAAT TCCCAACAGG GACCTACCCC GGCCTCCGCT CAGGAACGA TTCAAACTACT TCCCAAAGAAT TCTTCAGTGG AAGGTAAACA GAATCTGGTG ATTAATATAG TTCTCAGTAG GAACCACCAC GAGGACCAA TTTTCTTCC AAAAGTTTGG ATGATCCTT CCTGAGAAGA ATGAGCACA ATTAATATAG TTCTCAGTAG GAACCACCAC GAGGAGCTCA TTTTCTTCC AAAAGTTTGG ATGATCCTT	ACCAGGACCC GAGAACCACA GETGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC CTCTCCCCTG CTCCGGGTAA ATGAGGATCC GTTAACGGTT ACCAACTACC TAGACTGGAT TCGTGACAAC ATGCGGCCGT GATACTACG TATGATCAGC CTCGACTGTG CCTTCTAGTT GCCAGCCATC TGTTGTTTGC CCCTCCCCCG TGCCTTCCTT GACCCTGGAA GGTGCCACTC CCACTGTCCT TCCCTAATAA AATGAGGAAA TTGCATCGAA TGGTTCGACT CCACTGTCCT TCCCTAATAA AATGAGGAAA TTGCATCGA TTGTCTGAGT AGGTGCATT CTATTCTGGG GGGTGGGGTG GGCCAGGACA GCAAGGGGG GGATTGGGAA GACAATAGCA GGCATCCCC AGCTTTGCTT CTCAATTTCT TATTTCCATA ATGAGAAAAA AAGGAAAATT AATTTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCCAAAAAG GATCCTTTAG AGACAGTGTT CTCTGCACA ATAAGGACAA ACATTATTCA GAGGGATAC CCAGAGCTGA GACTCCTAAG CCAGTGAGTG GCACAGCATA CTAGGGAGAA ATATGCTTGT CATCACCGAA GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCCCAACAG GATAGCAGA GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGCAGA GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG GCAGGAGCCA GGCAGAGCA TATAAGGTGA GTTGGACAC TCAGGGCTGC GATTTCGCCC CAAACCTAG GGCCAGACCA TATAAGGTGA GTTGGACAC TCAGGGCTGC GATTTCGCCC CAAACCTAC GGCCAGACCA TATAAGGTGA GTTGGACAC TCAGGGCTGC GATTTCGCCC CAAACCTACC GGCCAATCCTA GCGTGAACGC TCGCAAAATA TGGGGATTG CAAGAACGGA GACCTACCCT GGCCTCCCCT CAGGAACGG TTCAAGAATA TGGGGATTG CAAGAACGGA GACCTACCCT GGCCTCCCCT CAGGAACGA TTCAAGCTAT TCCAACAAC GATCTCCATT CCTGAGAGAA ACCACCACA CATTTCTCCC AAAAATTATAG TTCCAAGCAG GAACACCAC CCTGAGAACAC ACCTTCT AAAGGACAA ATTAATATAG TTCCAGCTT AAGACCTAT CCTGAGAAACA GAACCTGTT AAAGGACAA ATTAATATAG TTCTCAGTTG GAACCACAAC CCTGAGAAACA GAACCTGCT TAAAGGACAA ATTAATATAG TTCCAGTAG AGAACCCAAAC CCTGAGAACCAC ACCACACC TTTTCTCCC AAAAATTATAG TTCCAGTAG GAACCCAAAC CACCACCAC GAGGAGCTCA TTTTCTTCC AAAAGTTTGG ATGATCCCTT AAGACCTAT CACCAGGAACCAC ACCAGACCA CTTTAGACCT TAGACCTC TAGACCTTT AAAACTTATT CACCAGGAACCAC ACCAGACCA CTTTAGACCT TTGTCTCA

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209 210	GAATTTGAAA	GTGACACGTT	TTTCCCAGAA	ATTGATTTGG	GGAAATATAA	ACTTCTCCCA	4440
211	GAATACCCAG	GCGTCCTCTC	TGAGGTCCAG	GAGGAAAAAG	GCATCAAGTA	TAAGTTTGAA	4500
212 213	GTCTACGAGA	AGAAAGACTA	ACAGGAAGAT	GCTTTCAAGT	TCTCTGCTCC	CCTCCTAAAG	4560
214 215	CTATGCATTT	TTATAAGACC	ATGGGACTTT	TGCTGGCTTT	AGATCAGCCT	CGACTGTGCC	4620
216		CA COCA MOMO	mmcmmmcccc	omacacacama	OCTOTO COTTO	CCCMCCA ACC	4680
217 218	TICIAGIIGC	CAGCCATCTG	IIGIIIGCCC	CICCCCGIG	CCITCCITGA	CCCIGGAAGG	
219 220	TGCCACTCCC	ACTGTCCTTT	CCTAATAAAA	TGAGGAAATT	GCATCGCATT	GTCTGAGTAG	4740
221	GTGTCATTCT	ATTCTGGGGG	GTGGGGTGGG	GCAGGACAGC	AAGGGGGAGG	ATTGGGAAGA	4800
223	CAATAGCAGG	CATGCTGGGG	ATGCGGTGGG	CTCTATGGAA	CCAGCTGGGG	CTCGAGCTAC	4860
224 225	TAGCTTTGCT	TCTCAATTTC	TTATTTGCAT	AATGAGAAAA	AAAGGAAAAT	TAATTTTAAC	4920
226 227	ACCAATTCAG	TAGTTGATTG	AGCAAATGCG	TTGCCAAAAA	GGATGCTTTA	GAGACAGTGT	4980
228							
229 230	TCTCTGCACA	GATAAGGACA	AACATTATTC	AGAGGGAGTA	CCCAGAGCTG	AGACTCCTAA	5040
231 232	GCCAGTGAGT	GGCACAGCAT	TCTAGGGAGA	AATATGCTTG	TCATCACCGA	AGCCTGATTC	5100
233	CGTAGAGCCA	CACCTTGGTA	AGGGCCAATC	TGCTCACACA	GGATAGAGAG	GGCAGGAGCC	5160
235	AGGGCAGAGC	ATATAAGGTG	AGGTAGGATC	AGTTGCTCCT	CACATTTGCT	TCTGACATAG	5220
236 237	TTGTGTTGGG	AGCTTGGATC	GATCCTCTAT	GGTTGAACAA	GATGGATTGC	ACGCAGGTTC	5280
238 239	TCCGGCCGCT	TGGGTGGAGA	GGCTATTCGG	CTATGACTGG	GCACAACAGA	CAATCGGCTG	5340
240							
241 242	CTCTGATGCC	GCCGTGTTCC	GGCTGTCAGC	GCAGGGGCGC	CCGGTTCTTT	TTGTCAAGAC	5400
243 244	CGACCTGTCC	GGTGCCCTGA	ATGAACTGCA	GGACGAGGCA	GCGCGGCTAT	CGTGGCTGGC	5460
245	CACGACGGGC	GTTCCTTGCG	CAGCTGTGCT	CGACGTTGTC	ACTGAAGCGG	GAAGGGACTG	5520
246 247	GCTGCTATTG	GGCGAAGTGC	CGGGGCAGGA	TCTCCTGTCA	TCTCACCTTG	CTCCTGCCGA	5580
248 249	GAAAGTATCC	ATCATGGCTG	ATGCAATGCG	GCGGCTGCAT	ACGCTTGATC	CGGCTACCTG	5640
250 251	CCCATTCCAC	CACCAACCGA	እ እ ር እ ጥርር ር እ ጥ	CCACCCACCA	ССТРСТСССР	TGGAAGCCGG	5700
252							• • • • • • • • • • • • • • • • • • • •
253 254	TCTTGTCGAT	CAGGATGATC	TGGACGAAGA	GCATCAGGGG	CTCGCGCCAG	CCGAACTGTT	5760
255 256	CGCCAGGCTC	AAGGCGCGCA	TGCCCGACGG	CGAGGATCTC	GTCGTGACCC	ATGGCGATGC	5820
257	CTGCTTGCCG	AATATCATGG	TGGAAAATGG	CCGCTTTTCT	GGATTCATCG	ACTGTGGCCG	5880
258 259	GCTGGGTGTG	GCGGACCGCT	ATCAGGACAT	AGCGTTGGCT	ACCCGTGATA	TTGCTGAAGA	5940
260 -							

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261 262	GCTTGGCGGC	GAATGGGCTG	ACCGCTTCCT	CGTGCTTTAC	GGTATCGCCG	CTCCCGATTC	6000
263	GCAGCGCATC	GCCTTCTATC	GCCTTCTTGA	CGAGTTCTTC	TGAGCGGGAC	TCTGGGGTTC	6060
264 265	GAAATGACCG	ACCAAGCGAC	GCCCAACCTG	CCATCACGAG	ATTTCGATTC	CACCGCCGCC	6120
266 267	TTCTATGAAA	GGTTGGGCTT	CGGAATCGTT	TTCCGGGACG	CCGGCTGGAT	GATCCTCCAG	6180
268							
269 270	CGCGGGGATC	TCATGCTGGA	GTTCTTCGCC	CACCCCAACT	TGTTTATTGC	AGCTTATAAT	6240
271 272	GGTTACAAAT	AAAGCAATAG	CATCACAAAT	TTCACAAATA	AAGCATTTTT	TTCACTGCAT	6300
273	TCTAGTTGTG	GTTTGTCCAA	ACTCATCAAT	CTATCTTATC	ATGTCTGGAT	CGCGGCCGCG	6360
274	>===========	03.00mm0000	m>>ma>maa	a			6400
275 276	ATCCCGTCGA	GAGCTTGGCG	TAATCATGGT	CATAGCTGTT	TCCTGTGTGA	AATTGTTATC	6420
277	CGCTCACAAT	TCCACACAAC	ATACGAGCCG	GAAGCATAAA	GTGTAAAGCC	теесетесст	6480
278					01011111000	100001001	0100
279	AATGAGTGAG	CTAACTCACA	TTAATTGCGT	TGCGCTCACT	GCCCGCTTTC	CAGTCGGGAA	6540
280							
281	ACCTGTCGTG	CCAGCTGCAT	TAATGAATCG	GCCAACGCGC	GGGGAGAGGC	GGTTTGCGTA	6600
282	mmaaaaaaama	mmeceemmee	macamas ama	`			
283 284	TIGGGCGCTC	TTCCGCTTCC	TCGCTCACTG	ACTCGCTGCG	CTCGGTCGTT	CGGCTGCGGC	6660
285	GAGCGGTATC	AGCTCACTCA	AAGGCGGTAA	TACGGTTATC	CACAGAATCA	GGGGATAACG	6720
286							0.20
287	CAGGAAAGAA	CATGTGAGCA	AAAGGCCAGC	AAAAGGCCAG	GAACCGTAAA	AAGGCCGCGT	6780
288							
289	TGCTGGCGTT	TTTCCATAGG	CTCCGCCCCC	CTGACGAGCA	TCACAAAAAT	CGACGCTCAA	6840
290	CDC2 C2 CCDC	6661116666		*********			6000
291 292	GTCAGAGGTG	GCGAAACCCG	ACAGGACTAT	AAAGATACCA	GGCGTTTCCC	CCTGGAAGCT	6900
293	CCCTCGTGCG	CTCTCCTGTT	CCGACCCTGC	CGCTTACCGG	ATACCTGTCC	GCCTTTCTCC	6960
294							
295	CTTCGGGAAG	CGTGGCGCTT	TCTCAATGCT	CACGCTGTAG	GTATCTCAGT	TCGGTGTAGG	7020
296					•		
297	TCGTTCGCTC	CAAGCTGGGC	TGTGTGCACG	AACCCCCCGT	TCAGCCCGAC	CGCTGCGCCT	7080
298 299	ጥ ልጥሮርርር ሞል ል	CTATCGTCTT	CACTCCAACC	CCCTAACACA	CC A CTTTA TICC	CCACTCCCAC	7140
300	INICCOGIAN	CIMICGICII	GAGICCAACC	CGGTAAGACA	CGACTIATCG	CCACIGGCAG	/140
301	CAGCCACTGG	TAACAGGATT	AGCAGAGCGA	GGTATGTAGG	CGGTGCTACA	GAGTTCTTGA	7200
302							
303	AGTGGTGGCC	TAACTACGGC	TACACTAGAA	GGACAGTATT	TGGTATCTGC	GCTCTGCTGA	7260
304							
305 306	AGCCAGTTAC	CTTCGGAAAA	AGAGTTGGTA	GCTCTTGATC	CGGCAAACAA	ACCACCGCTG	7320
307	GTAGCGGTGG	TTTTTTTGTT	ТССАВССАСС	AGATTACCCC	CDCDDDDDD	ССАТСТСААС	7380
308	-1		200111001100		VIIVII IIIIMM	Contolond	, 500
309	AAGATCCTTT	GATCTTTTCT	ACGGGGTCTG	ACGCTCAGTG	GAACGAAAAC	TCACGTTAAG	7440
310							
311	GGATTTTGGT	CATGAGATTA	TCAAAAAGGA	TCTTCACCTA	GATCCTTTTA	AATTAAAAAT	7500
312							

363

364 (iv)ANTI-SENSE: no

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313	GAAGTTTTAA	ATCAATCTAA	AGTATATATG	AGTAAACTTG	GTCTGACAGT	TACCAATGCT	7560
314							
315	TAATCAGTGA	GGCACCTATC	TCAGCGATCT	GTCTATTTCG	TTCATCCATA	GTTGCCTGAC	7620
316 317	mcccccmccm	GTAGATAACT	ACCAMA CCCC	NCCCCOMMN CC	3 momocoooo	3.0mc.cmc.c3.3	7680
317	TCCCCGTCGT	GIAGAIAACI	ACGATACGGG	AGGGCTTACC	ATCTGGCCCC	AGTGCTGCAA	7680
319	тсатассесе	AGACCCACGC	тересесте	САСАФФФАТС	ассаатааас	CACCCACCCC	7740
320	10.11.100000		10110000010	Onomitanto	ndchilmine	CAGCCAGCCG	,,40
321	GAAGGGCCGA	GCGCAGAAGT	GGTCCTGCAA	CTTTATCCGC	CTCCATCCAG	TCTATTAATT	7800
322							
323	GTTGCCGGGA	AGCTAGAGTA	AGTAGTTCGC	CAGTTAATAG	TTTGCGCAAC	GTTGTTGCCA	7860
324							
325	TTGCTACAGG	CATCGTGGTG	TCACGCTCGT	CGTTTGGTAT	GGCTTCATTC	AGCTCCGGTT	7920
326			•				
327	CCCAACGATC	AAGGCGAGTT	ACATGATCCC	CCATGTTGTG	CAAAAAAGCG	GTTAGCTCCT	7980
328	macamaamaa	03.maammama	2022002200	maaaaaaaa		3.0000000000000000000000000000000000000	0040
329 330	TEGGTEETEE	GATCGTTGTC	AGAAGTAAGT	TGGCCGCAGT	GTTATCACTC	ATGGTTATGG	8040
331	СРССРСТССР	TAATTCTCTT	ъ Статсътас	САТСССТААС	አ ጥር ርጥጥጥጥርጥ	CTC A CTC CTC	8100
332	011001101011		HOIGICHIGO	CHICCGIANG	AIGCIIIICI	GIGACIGGIG	0100
333	AGTACTCAAC	CAAGTCATTC	TGAGAATAGT	GTATGCGGCG	ACCGAGTTGC	TCTTGCCCGG	8160
334							
335	CGTCAATACG	GGATAATACC	GCGCCACATA	GCAGAACTTT	AAAAGTGCTC	ATCATTGGAA	8220
336							
337	AACGTTCTTC	GGGGCGAAAA	CTCTCAAGGA	TCTTACCGCT	GTTGAGATCC	AGTTCGATGT	8280
338	***********						
339	AACCCACTCG	TGCACCCAAC	TGATCTTCAG	CATCTTTTAC	TTTCACCAGC	GTTTCTGGGT	8340
340 341	CACCAAAAAC	AGGAAGGCAA	እአጥሮሮሮሮሮአአ	******************	3 3 C C C C C 3 C 3	CCCAAACCCC	8400
342	GAGCAAAAAC	NGGNAGGCAA	ANTOCCOCAN	AAAAGGGAAI	ANGGGCGACA	CGGAAATGII	8400
343	GAATACTCAT	ACTCTTCCTT	TTTCAATATT	ATTGAAGCAT	TTATCAGGGT	TATTGTCTCA	8460
344							
345	TGAGCGGATA	CATATTTGAA	TGTATTTAGA	AAAATAAACA	AATAGGGGTT	CCGCGCACAT	8520
346							
347	TTCCCCGAAA	AGTGCCACCT	8540				
348							
349							
350	(2) TNEODY2 MT/	ON EOD CEO	TD NO - 1	n .			
351 352	(3) INFORMATION	on for Seq.	ID. NO.: 4	2:			
353	(i)SEQUENCE (ייים ד מתייים ממממיי	TTCS.				
354	(I)DDQODMCD (1100.				
355	(A) LENGTH: 9	9209 bases					
356	(B) TYPE: nuc						
357	(C)STRANDEDNI		9				
358	(D) TOPOLOGY:	circular					
359							
360	(ii)MOLECULE	TYPE: DNA	(genomic)				
361	/						
362 363	(iii) HYPOTHET	rical: yes					

365

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366 367	(ix)SEQUENCE	DESCRIPTION	N: SEQ. ID	. NO.: 2:			
368 369 370	GACGTCGCGG	CCGCTCTAGG	CCTCCAAAAA	AGCCTCCTCA	CTACTTCTGG	AATAGCTCAG	60
371 372	AGGCCGAGGC	GGCCTCGGCC	TCTGCATAAA	TAAAAAAAT	TAGTCAGCCA	TGCATGGGGC	120
373 374	GGAGAATGGG	CGGAACTGGG	CGGAGTTAGG	GGCGGGATGG	GCGGAGTTAG	GGGCGGGACT	180
375 376		ACTAATTGAG					240
377 378		ACCTGGTTGC					300
379 380		GGGACTTTCC					360
381 382		AGTAATCAAT					420
383 384 385						CCGCCCATTG	480
386 387		ATTTACGGTA				TCATATCCCA	540 600
388 389		CTATTGACGT					660
390 391		GGGACTTTCC					720
392 393		GGTTTTGGCA					780
394 395	TTTCCAAGTC	TCCACCCCAT	TGACGTCAAT	GGGAGTTTGT	TTTGGCACCA	AAATCAACGG	840
396 397	GACTTTCCAA	AATGTCGTAA	CAACTCCGCC	CCATTGACGC	AAATGGGCGG	TAGGCGTGTA	900
398 399 400	CGGTGGGAGG	TCTATATAAG	CAGAGCTGGG	TACGTGAACC	GTCAGATCGC	CTGGAGACGC	960
400 401 402	CATCACAGAT	CTCTCACTAT	GGATTTTCAG	GTGCAGATTA	TCAGCTTCCT	GCTAATCAGT	1020
403 404	GCTTCAGTCA	TAATGTCCAG	AGGACAAATT	GTTCTCTCCC	AGTCTCCAGC	AATCCTGTCT	1080
405 406	GCATCTCCAG	GGGAGAAGGT	CACAATGACT	TGCAGGGCCA	GCTCAAGTGT	AAGTTACATC	1140
407 408	CACTGGTTCC	AGCAGAAGCC	AGGATCCTCC	CCCAAACCCT	GGATTTATGC	CACATCCAAC	1200
409 410	CTGGCTTCTG	GAGTCCCTGT	TCGCTTCAGT	GGCAGTGGGT	CTGGGACTTC	TTACTCTCTC	1260
411 412	ACAATCAGCA	GAGTGGAGGC	TGAAGATGCT	GCCACTTATT	ACTGCCAGCA	GTGGACTAGT	1320
413 414						GGCTGCACCA	1380
415 416	TCTGTCTTCA	TCTTCCCGCC	ATCTGATGAG	CAGTTGAAAT	CTGGAACTGC	CTCTGTTGTG	1440

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417 418	TGCCTGCTGA	ATAACTTCTA	TCCCAGAGAG	GCCAAAGTAC	AGTGGAAGGT	GGATAACGCC	1500
419 420	CTCCAATCGG	GTAACTCCCA	GGAGAGTGTC	ACAGAGCAGG	ACAGCAAGGA	CAGCACCTAC	1560
421	AGCCTCAGCA	GCACCCTGAC	GCTGAGCAAA	GCAGACTACG	AGAAACACAA	AGTCTACGCC	1620
422 423	TGCGAAGTCA	CCCATCAGGG	CCTGAGCTCG	CCCGTCACAA	AGAGCTTCAA	CAGGGGAGAG	1680
424 425	TGTTGAATTC	AGATCCGTTA	ACGGTTACCA	ACTACCTAGA	CTGGATTCGT	GACAACATGC	1740
426 427	GGCCGTGATA	TCTACGTATG	ATCAGCCTCG	ACTGTGCCTT	CTAGTTGCCA	GCCATCTGTT	1800
428 429	GTTTGCCCCT	CCCCGTGCC	TTCCTTGACC	CTGGAAGGTG	CCACTCCCAC	TGTCCTTTCC	1860
430 431	TAATAAAATG	AGGAAATTGC	ATCGCATTGT	CTGAGTAGGT	GTCATTCTAT	TCTGGGGGGT	1920
432 433	GGGGTGGGGC	AGGACAGCAA	GGGGGAGGAT	TGGGAAGACA	ATAGCAGGCA	TGCTGGGGAT	1980
434 435	GCGGTGGGCT	CTATGGAACC	AGCTGGGGCT	CGACAGCTAT	GCCAAGTACG	CCCCTATTG	2040
436 437	ACGTCAATGA	CGGTAAATGG	CCCGCCTGGC	ATTATGCCCA	GTACATGACC	TTATGGGACT	2100
438 439	TTCCTACTTG	GCAGTACATC	TACGTATTAG	TCATCGCTAT	TACCATGGTG	ATGCGGTTTT	2160
440 441	GGCAGTACAT	CAATGGGCGT	GGATAGCGGT	TTGACTCACG	GGGATTTCCA	AGTCTCCACC	2220
442 443		CAATGGGAGT				·	2280
444							
445 446	GTAACAACTC	CGCCCCATTG	ACGCAAATGG	GCGGTAGGCG	TGTACGGTGG	GAGGTCTATA	2340
447 448	TAAGCAGAGC	TGGGTACGTC	CTCACATTCA	GTGATCAGCA	CTGAACACAG	ACCCGTCGAC	2400
449 450	ATGGGTTGGA	GCCTCATCTT	GCTCTTCCTT	GTCGCTGTTG	CTACGCGTGT	CCTGTCCCAG	2460
451 452	GTACAACTGC	AGCAGCCTGG	GGCTGAGCTG	GTGAAGCCTG	GGGCCTCAGT	GAAGATGTCC	2520
453 454	TGCAAGGCTT	CTGGCTACAC	ATTTACCAGT	TACAATATGC	ACTGGGTAAA	ACAGACACCT	2580
455 456	GGTCGGGGCC	TGGAATGGAT	TGGAGCTATT	TATCCCGGAA	ATGGTGATAC	TTCCTACAAT	2640
457	CAGAAGTTCA	AAGGCAAGGC	CACATTGACT	GCAGACAAAT	CCTCCAGCAC	AGCCTACATG	2700
458 459	CAGCTCAGCA	GCCTGACATC	TGAGGACTCT	GCGGTCTATT	ACTGTGCAAG	ATCGACTTAC	2760
460 461	TACGGCGGTG	ACTGGTACTT	CAATGTCTGG	GGCGCAGGGA	CCACGGTCAC	CGTCTCTGCA	2820
462 463	GCTAGCACCA	AGGGCCCATC	GGTCTTCCCC	CTGGCACCCT	CCTCCAAGAG	CACCTCTGGG	2880
464 465	GGCACAGCGG	CCCTGGGCTG	CCTGGTCAAG	GACTACTTCC	CCGAACCGGT	GACGGTGTCG	2940
466 467	TGGAACTCAG	GCGCCCTGAC	CAGCGGCGTG	CACACCTTCC	CGGCTGTCCT	ACAGTCCTCA	3000
468							

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469	GGACTCTACT	CCCTCAGCAG	CGTGGTGACC	GTGCCCTCCA	GCAGCTTGGG	CACCCAGACC	3060
470 471	TACATCTGCA	ACGTGAATCA	CAAGCCCAGC	AACACCAAGG	TGGACAAGAA	AGCAGAGCCC	3120
472 473	AAATCTTGTG	ACAAAACTCA	CACATGCCCA	CCGTGCCCAG	CACCTGAACT	CCTGGGGGGA	3180
474 475 476	CCGTCAGTCT	TCCTCTTCCC	CCCAAAACCC	AAGGACACCC	TCATGATCTC	CCGGACCCCT	3240
477 478	GAGGTCACAT	GCGTGGTGGT	GGACGTGAGC	CACGAAGACC	CTGAGGTCAA	GTTCAACTGG	3300
479 480	TACGTGGACG	GCGTGGAGGT	GCATAATGCC	AAGACAAAGC	CGCGGGAGGA	GCAGTACAAC	3360
481 482	AGCACGTACC	GTGTGGTCAG	CGTCCTCACC	GTCCTGCACC	AGGACTGGCT	GAATGGCAAG	3420
483 484	GAGTACAAGT	GCAAGGTCTC	CAACAAAGCC	CTCCCAGCCC	CCATCGAGAA	AACCATCTCC	3480
485 486	AAAGCCAAAG	GGCAGCCCCG	AGAACCACAG	GTGTACACCC	TGCCCCCATC	CCGGGATGAG	3540
487 488	CTGACCAAGA	ACCAGGTCAG	CCTGACCTGC	CTGGTCAAAG	GCTTCTATCC	CAGCGACATC	3600
489 490	GCCGTGGAGT	GGGAGAGCAA	TGGGCAGCCG	GAGAACAACT	ACAAGACCAC	GCCTCCCGTG	3660
491 492	CTGGACTCCG	ACGGCTCCTT	CTTCCTCTAC	AGCAAGCTCA	CCGTGGACAA	GAGCAGGTGG	3720
493 494	CAGCAGGGGA	ACGTCTTCTC	ATGCTCCGTG	ATGCATGAGG	CTCTGCACAA	CCACTACACG	3780
495 496	CAGAAGAGCC	TCTCCCTGTC	TCCGGGTAAA	TGAGGATCCG	TTAACGGTTA	CCAACTACCT	3840
497 498	AGACTGGATT	CGTGACAACA	TGCGGCCGTG	ATATCTACGT	ATGATCAGCC	TCGACTGTGC	3900
499 500	CTTCTAGTTG	CCAGCCATCT	GTTGTTTGCC	CCTCCCCGT	GCCTTCCTTG	ACCCTGGAAG	3960
501 502	GTGCCACTCC	CACTGTCCTT	TCCTAATAAA	ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	4020
503 504	GGTGTCATTC	TATTCTGGGG	GGTGGGGTGG	GGCAGGACAG	CAAGGGGGAG	GATTGGGAAG	4080
505 506	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	GCTCTATGGA	ACCAGCTGGG	GCTCGACAGC	4140
507 508	GCTGGATCTC	CCGATCCCCA	GCTTTGCTTC	TCAATTTCTT	ATTTGCATAA	TGAGAAAAA	4200
509 510	AGGAAAATTA	ATTTTAACAC	CAATTCAGTA	GTTGATTGAG	CAAATGCGTT	GCCAAAAAGG	4260
511 512	ATGCTTTAGA	GACAGTGTTC	TCTGCACAGA	TAAGGACAAA	CATTATTCAG	AGGGAGTACC	4320
513 514	CAGAGCTGAG	ACTCCTAAGC	CAGTGAGTGG	CACAGCATTC	TAGGGAGAAA	TATGCTTGTC	4380
515 516	ATCACCGAAG	CCTGATTCCG	TAGAGCCACA	CCTTGGTAAG	GGCCAATCTG	CTCACACAGG	4440
517 518	ATAGAGAGGG	CAGGAGCCAG	GGCAGAGCAT	ATAAGGTGAG	GTAGGATCAG	TTGCTCCTCA	4500
519 520	CATTTGCTTC	TGACATAGTT	GTGTTGGGAG	CTTGGATAGC	TTGGACAGCT	CAGGGCTGCG	4560

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521 522	ATTTCGCGCC	AAACTTGACG	GCAATCCTAG	CGTGAAGGCT	GGTAGGATTT	TATCCCCGCT	4620
523	GCCATCATGG	TTCGACCATT	GAACTGCATC	GTCGCCGTGT	CCCAAAATAT	GGGGATTGGC	4680
524 525	AAGAACGGAG	ACCTACCCTG	GCCTCCGCTC	AGGAACGAGT	TCAAGTACTT	CCAAAGAATG	4740
526 527	ACCACAACCT	CTTCAGTGGA	AGGTAAACAG	AATCTGGTGA	TTATGGGTAG	GAAAACCTGG	4800
528 529	TTCTCCATTC	CTGAGAAGAA	TCGACCTTTA	AAGGACAGAA	TTAATATAGT	TCTCAGTAGA	4860
530 531	GAACTCAAAG	AACCACCACG	AGGAGCTCAT	TTTCTTGCCA	AAAGTTTGGA	TGATGCCTTA	4920
532 533	AGACTTATTG	AACAACCGGA	ATTGGCAAGT	AAAGTAGACA	TGGTTTGGAT	AGTCGGAGGC	4980
534 535		ACCAGGAAGC					5040
536 537		AATTTGAAAG					5100
538							
539 540	CTTCTCCCAG	AATACCCAGG	CGTCCTCTCT	GAGGTCCAGG	AGGAAAAAGG	CATCAAGTAT	5160
541 542	AAGTTTGAAG	TCTACGAGAA	GAAAGACTAA	CAGGAAGATG	CTTTCAAGTT	CTCTGCTCCC	5220
543 544	CTCCTAAAGC	TATGCATTTT	TATAAGACCA	TGGGACTTTT	GCTGGCTTTA	GATCAGCCTC	5280
545 546	GACTGTGCCT	TCTAGTTGCC	AGCCATCTGT	TGTTTGCCCC	TCCCCCGTGC	CTTCCTTGAC	5340
547 548	CCTGGAAGGT	GCCACTCCCA	CTGTCCTTTC	CTAATAAAAT	GAGGAAATTG	CATCGCATTG	5400
549	TCTGAGTAGG	TGTCATTCTA	TTCTGGGGGG	TGGGGTGGGG	CAGGACAGCA	AGGGGGAGGA	5460
550 551	TTGGGAAGAC	AATAGCAGGC	ATGCTGGGGA	TGCGGTGGGC	TCTATGGAAC	CAGCTGGGGC	5520
552 553	TCGAGCTACT	AGCTTTGCTT	CTCAATTTCT	TATTTGCATA	ATGAGAAAAA	AAGGAAAATT	5580
554 555	AATTTTAACA	CCAATTCAGT	AGTTGATTGA	GCAAATGCGT	TGCCAAAAAG	GATGCTTTAG	5640
556 557	AGACAGTGTT	CTCTGCACAG	ATAAGGACAA	ACATTATTCA	GAGGGAGTAC	CCAGAGCTGA	5700
558 559		CCAGTGAGTG					5760
560 561							
562		GTAGAGCCAC					5820
563 564		GGGCAGAGCA					5880
565 566	CTGACATAGT	TGTGTTGGGA	GCTTGGATCG	ATCCTCTATG	GTTGAACAAG	ATGGATTGCA	5940
567 568	CGCAGGTTCT	CCGGCCGCTT	GGGTGGAGAG	GCTATTCGGC	TATGACTGGG	CACAACAGAC	6000
569 570	AATCGGCTGC	TCTGATGCCG	CCGTGTTCCG	GCTGTCAGCG	CAGGGGCGCC	CGGTTCTTTT	6060
571 572	TGTCAAGACC	GACCTGTCCG	GTGCCCTGAA	TGAACTGCAG	GACGAGGCAG	CGCGGCTATC	6120
512							

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573 574	GTGGCTGGCC	ACGACGGGCG	TTCCTTGCGC	AGCTGTGCTC	GACGTTGTCA	CTGAAGCGGG	6180
575 576	AAGGGACTGG	CTGCTATTGG	GCGAAGTGCC	GGGGCAGGAT	CTCCTGTCAT	CTCACCTTGC	6240
57 7 578	TCCTGCCGAG	AAAGTATCCA	TCATGGCTGA	TGCAATGCGG	CGGCTGCATA	CGCTTGATCC	6300
579 580	GGCTACCTGC	CCATTCGACC	ACCAAGCGAA	ACATCGCATC	GAGCGAGCAC	GTACTCGGAT	6360
581 582	GGAAGCCGGT	CTTGTCGATC	AGGATGATCT	GGACGAAGAG	CATCAGGGGC	TCGCGCCAGC	6420
583 584	CGAACTGTTC	GCCAGGCTCA	AGGCGCGCAT	GCCCGACGGC	GAGGATCTCG	TCGTGACCCA	6480
585 586	TGGCGATGCC	TGCTTGCCGA	ATATCATGGT	GGAAAATGGC	CGCTTTTCTG	GATTCATCGA	6540
587 588	CTGTGGCCGG	CTGGGTGTGG	CGGACCGCTA	TCAGGACATA	GCGTTGGCTA	CCCGTGATAT	6600
589 590	TGCTGAAGAG	CTTGGCGGCG	AATGGGCTGA	CCGCTTCCTC	GTGCTTTACG	GTATCGCCGC	6660
591 592	TCCCGATTCG	CAGCGCATCG	CCTTCTATCG	CCTTCTTGAC	GAGTTCTTCT	GAGCGGGACT	6720
593 594	CTGGGGTTCG	AAATGACCGA	CCAAGCGACG	CCCAACCTGC	CATCACGAGA	TTTCGATTCC	6780
595 596	ACCGCCGCCT	TCTATGAAAG	GTTGGGCTTC	GGAATCGTTT	TCCGGGACGC	CGGCTGGATG	6840
597 598	ATCCTCCAGC	GCGGGGATCT	CATGCTGGAG	TTCTTCGCCC	ACCCCAACTT	GTTTATTGCA	6900
599 600	GCTTATAATG	GTTACAAATA	AAGCAATAGC	ATCACAAATT	TCACAAATAA	AGCATTTTTT	6960
601 602	TCACTGCATT	CTAGTTGTGG	TTTGTCCAAA	CTCATCAATC	TATCTTATCA	TGTCTGGATC	7020
603 604	GCGGCCGCGA	TCCCGTCGAG	AGCTTGGCGT	AATCATGGTC	ATAGCTGTTT	CCTGTGTGAA	7080
605 606	ATTGTTATCC	GCTCACAATT	CCACACAACA	TACGAGCCGG	AAGCATAAAG	TGTAAAGCCT	7140
607 608	GGGGTGCCTA	ATGAGTGAGC	TAACTCACAT	TAATTGCGTT	GCGCTCACTG	CCCGCTTTCC	7200
609 610	AGTCGGGAAA	CCTGTCGTGC	CAGCTGCATT	AATGAATCGG	CCAACGCGCG	GGGAGAGGCG	7260
611 612	GTTTGCGTAT	TGGGCGCTCT	TCCGCTTCCT	CGCTCACTGA	CTCGCTGCGC	TCGGTCGTTC	7320
613 614	GGCTGCGGCG	AGCGGTATCA	GCTCACTCAA	AGGCGGTAAT	ACGGTTATCC	ACAGAATCAG	7380
615 616	GGGATAACGC	AGGAAAGAAC	ATGTGAGCAA	AAGGCCAGCA	AAAGGCCAGG	AACCGTAAAA	7440
617 618	AGGCCGCGTT	GCTGGCGTTT	TTCCATAGGC	TCCGCCCCCC	TGACGAGCAT	CACAAAAATC	7500
619 620	GACGCTCAAG	TCAGAGGTGG	CGAAACCCGA	CAGGACTATA	AAGATACCAG	GCGTTTCCCC	7560
621 622	CTGGAAGCTC	CCTCGTGCGC	TCTCCTGTTC	CGACCCTGCC	GCTTACCGGA	TACCTGTCCG	7620
623 624	CCTTTCTCCC	TTCGGGAAGC	GTGGCGCTTT	CTCAATGCTC	ACGCTGTAGG	TATCTCAGTT	7680

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625 626	CGGTGTAGGT	CGTTCGCTCC	AAGCTGGGCT	GTGTGCACGA	ACCCCCCGTT	CAGCCCGACC	7740
627 628	GCTGCGCCTT	ATCCGGTAAC	TATCGTCTTG	AGTCCAACCC	GGTAAGACAC	GACTTATCGC	7800
629 630	CACTGGCAGC	AGCCACTGGT	AACAGGATTA	GCAGAGCGAG	GTATGTAGGC	GGTGCTACAG	7860
631 632	AGTTCTTGAA	GTGGTGGCCT	AACTACGGCT	ACACTAGAAG	GACAGTATTT	GGTATCTGCG	7920
633 634	CTCTGCTGAA	GCCAGTTACC	TTCGGAAAAA	GAGTTGGTAG	CTCTTGATCC	GGCAAACAAA	7980
635 636		TAGCGGTGGT					8040
637 638		AGATCCTTTG					8100
639 640		GATTTTGGTC					8160
641 642 643		AAGTTTTAAA					8220
644 645		AATCAGTGAG					8280 8340
646 647		GATACCGCGA					8400
648 649		AAGGGCCGAG					8460
650 651		TTGCCGGGAA					8520
652 653	TTGTTGCCAT	TGCTACAGGC	ATCGTGGTGT	CACGCTCGTC	GTTTGGTATG	GCTTCATTCA	8580
654 655	GCTCCGGTTC	CCAACGATCA	AGGCGAGTTA	CATGATCCCC	CATGTTGTGC	AAAAAAGCGG	8640
656 657	TTAGCTCCTT	CGGTCCTCCG	ATCGTTGTCA	GAAGTAAGTT	GGCCGCAGTG	TTATCACTCA	8700
658 659	TGGTTATGGC	AGCACTGCAT	AATTCTCTTA	CTGTCATGCC	ATCCGTAAGA	TGCTTTTCTG	8760
660 661 662	TGACTGGTGA	GTACTCAACC	AAGTCATTCT	GAGAATAGTG	TATGCGGCGA	CCGAGTTGCT	8820
663 664	CTTGCCCGGC	GTCAATACGG	GATAATACCG	CGCCACATAG	CAGAACTTTA	AAAGTGCTCA	8880
665 666	TCATTGGAAA	ACGTTCTTCG	GGGCGAAAAC	TCTCAAGGAT	CTTACCGCTG	TTGAGATCCA	8940
667 668	GTTCGATGTA	ACCCACTCGT	GCACCCAACT	GATCTTCAGC	ATCTTTTACT	TTCACCAGCG	9000
669 670	TTTCTGGGTG	AGCAAAAACA	GGAAGGCAAA	ATGCCGCAAA	AAAGGGAATA	AGGGCGACAC	9060
671 672	GGAAATGTTG	AATACTCATA	CTCTTCCTTT	TTCAATATTA	TTGAAGCATT	TATCAGGGTT	9120
673 674	ATTGTCTCAT	GAGCGGATAC	ATATTTGAAT	GTATTTAGAA	AAATAAACAA	ATAGGGGTTC	9180
675 676	CGCGCACATT	TCCCCGAAAA	GTGCCACCT				9209

677

(4) INFORMATION FOR SEQ. ID. NO.: 3:

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```
678
679
     (i) SEQUENCE CHARACTERISTICS:
680
681
     (A) LENGTH: 54 bases
    (B) TYPE: nucleic acid
682
    (C)STRANDEDNESS: single
683
684
    (D) TOPOLOGY: linear
                                                                 Place as the place of the form ber.
685
686
    (ii) MOLECULE TYPE: DNA (genomic)
687
688
    (iii) HYPOTHETICAL: yes
689
    (iv)ANTI-SENSE: no
690
691
692
    (ix) SEQUENCE DESCRIPTION: SEQ. | ID. NO.: 3:
693
694
    5' ATC ACA GAT CTC TCA CCA TGG ATT TTC AGG TBC AGA TTA TCA GCT52
695
                     - This number heeds to
696
              e invalia
697
     (5) INFORMATION FOR SEQ. ID. NO.: 4:
698
699
    (i) SEQUENCE CHARACTERISTICS:
700
701
702
    (A) LENGTH: 30 bases
703
    (B) TYPE: nucleic acid
704
    (C)STRANDEDNESS: single
705
    (D) TOPOLOGY: linear
706
707
     (ii) MOLECULE TYPE: DNA (genomic)
708
709
    (iii) HYPOTHETICAL: yes
    (iv) ANTI-SENSE: yes - the above anti-sense is "no". Prease ver, Ey
710
711
                                                           PTO assumes
                                these responses.
712
713
    (ix) SEQUENCE DESCRIPTION: SEQ. ID. NO.: 4:
714
715
716
       TGC AGC ATC CGT ACG TTT GAT TTC CAG CTT/3'BO
717
718
719
     (6) INFORMATION FOR SEQ. ID. NO.: 5:
720
721
    (i) SEQUENCE CHARACTERISTICS:
722
723
    (A)LENGTH: 384 bases
724
     (B) TYPE: nucleic acid
725
     (C)STRANDEDNESS: single
    (D)TOPOLOGY: linear
726
727
728
    (ii) MOLECULE TYPE: DNA (genomic)
```

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-space

```
729
730
     (iii) HYPOTHETICAL: yes
731
732
     (iv)ANTI-SENSE: no
733
     (ix) SEQUENCE DESCRIPTION: SEQ. ID. NO.: 5:
734
735
736
       ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC 51
737
738
       ATA ATG TCC AGA GGG CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT102_
739
740
       GCA TCT CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA153
741
742
      AGT TAC ATC CAC TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG204-
743
744
      ATT TAT GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC255
745
746
      AGT GGG TCT GGG ACT TCT TAC TCT CTC ACA ATC AGC AGA GTG GAG GCT GAR306
747
748
       GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG ACT AGT AAC CCA CCC ACG TTC357
749
750
       GGA GGG GGG ACC AAG CTG GAA ATC AAA384
751
752
753
754
     (7) INFORMATION FOR SEQ. ID. NO.: 6:
755
756
    (i) SEQUENCE CHARACTERISTICS:
757
758
     (A) LENGTH: 27 bases
759
     (B) TYPE: nucleic acid
760
     (C)STRANDEDNESS: single
761
     (D) TOPOLOGY: linear
762
763
     (ii)MOLECULE TYPE: DNA (genomic)
764
765
     (iii) HYPOTHETICAL:
                         yes
766
767
     (iv)ANTI-SENSE: no
768
     (ix) SEQUENCE DESCRIPTION:
769
                                 SEQ. ID. NO.: 6:
770
771
       GCG GCT CCC ACG CGT GTC CTG TCC CAG 3 27
772
773
774
775
776
     (8) INFORMATION FOR SEQ. ID. NO.: 7:
777
778
779
     (i) SEQUENCE CHARACTERISTICS:
```

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```
781
    (A)LENGTH: 29 bases
782
     (B) TYPE: nucleic acid
     (C)STRANDEDNESS: single
783
784
     (D) TOPOLOGY: linear
785
786
     (ii)MOLECULE TYPE: DNA (genomic)
787
    (iii) HYPOTHETICAL: yes
788
789
790 (iv) ANTI-SENSE: yes
791
    (ix) SEQUENCE DESCRIPTION: SEQ. ID. NO.:
792
793
794 5' GG(G/C), TGT TGT GCT AGC TG'(A/C) (A/G)GA GAC (G/A)GT GA (3')29
795
                                                                     in the feature table (ix) feature:
                asid define the alternatives
796 USe
     (9) INFORMATION FOR SEQ. ID. NO.: 8:
797
798
799
     (i) SEQUENCE CHARACTERISTICS:
800
     (A) LENGTH: 420 bases
801
     (B) TYPE: nucleic acid
802
803
     (C)STRANDEDNESS: single
804
     (D) TOPOLOGY: linear
805
806
     (ii) MOLECULE TYPE: DNA (genomic)
807
808
    (iii) HYPOTHETICAL: yes
809
    (iv) ANTI-SENSE: no
810
811
812
     (ix) SEQUENCE DESCRIPTION: SEQ. ID. NO.: 8:
813
814
     ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT GTC 51
815
816
     CTG TCC CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG CCT GGG102
817
818
819
     GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT ACC AGT TAC153
820
821
     AAT ATG CAC TGG GTA AAA CAG ACA CCT GGT CGG GGC CTG GAA TGG ATT GGA 204-
822
     GCT ATT TAT CCC GGA AAT GGT GAT ACT TCC TAC AAT CAG AAG TTC AAA GGC255
823
824
     AAG GCC ACA TTG ACT GCA GAC AAA TCC TCC AGC ACA GCC TAC ATG CAG CTC306
825
826
     AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT TAC TGT GCA AGA TCG ACT357
827
828
829
     TAC TAC GGC GGT GAC TGG TAC TTC AAT GTC TGG GGC GCA GGG ACC ACG GTC408
830
     ACC GTC TCT GCA 420
831
```